

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/464,099DATE: 05/19/2000
TIME: 07:33:01

INPUT SET: S35499.raw

#8

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2

3 (1) General Information:

4
5 (i) APPLICANT: Barry, Gerard F.
6 Kishore, Ganesh M.
7 Padgette, Stephen R.
8 Stallings, William C.

9
10 (ii) TITLE OF INVENTION: Glyphosate Tolerant
11 5-Enolpyruvylshikimate-3-Phosphate Synthases

12
13 (iii) NUMBER OF SEQUENCES: 69

14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
17 (B) STREET: 700 Chesterfield Village Parkway
18 (C) CITY: St. Louis
19 (D) STATE: Missouri
20 (E) COUNTRY: USA
21 (F) ZIP: 63198

22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: 09/464,099
31 (B) FILING DATE:
32 (C) CLASSIFICATION:

33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 09/137,440
36 (B) FILING DATE:

37
38 (A) APPLICATION NUMBER: US 08/833,485
39 (B) FILING DATE: 07-APR-1997

40
41 (A) APPLICATION NUMBER: US 08/306,063
42 (B) FILING DATE: 13-SEP-1994

43
44 (vii) PRIOR APPLICATION DATA:
45 (A) APPLICATION NUMBER: US 07/749,611

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/464,099DATE: 05/19/2000
TIME: 07:33:02

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47 (B) FILING DATE: 28-AUG-1991
48
49
50 (vii) PRIOR APPLICATION DATA:
51 (A) APPLICATION NUMBER: US 07/576,537
52 (B) FILING DATE: 31-AUG-1990
53
54
55 (viii) ATTORNEY/AGENT INFORMATION:
56 (A) NAME: Hoerner Jr., Dennis R.
57 (B) REGISTRATION NUMBER: 30,914
58 (C) REFERENCE/DOCKET NUMBER: 38-21(15117)A
59
60 (ix) TELECOMMUNICATION INFORMATION:
61 (A) TELEPHONE: (314) 737-6099
62 (B) TELEFAX: (314) 737-6047
63
64
65 (2) INFORMATION FOR SEQ ID NO:1:
66
67 (i) SEQUENCE CHARACTERISTICS:
68 (A) LENGTH: 597 base pairs
69 (B) TYPE: nucleic acid
70 (C) STRANDEDNESS: double
71 (D) TOPOLOGY: linear
72
73 (ii) MOLECULE TYPE: DNA (genomic)
74
75
76
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
78
79 TCATCAAAAT ATTTAGCAGC ATTCCAGATT GGGTTCAATC AACAAAGGTAC GAGCCATATC 60
80
81 ACTTTATTCA AATTGGTATC GCCAAAACCA AGAAGGAACCT CCCATCCTCA AAGGTTTGTA 120
82
83 AGGAAGAAATT CTCAGTCCAA AGCCTCAACA AGGTCAAGGGT ACAGAGTCTC CAAACCATT 180
84
85 GCCAAAAGCT ACAGGAGATC AATGAAGAAT CTTCAATCAA AGTAAACTAC TGTTCCAGCA 240
86
87 CATGCATCAT GGTCAAGTAAAG TTTCAAGAAAA AGACATCCAC CGAAGACTTA AAGTTAGTGG 300
88
89 GCATCTTGA AAGTAATCTT GTCAACATCG AGCAGCTGGC TTGTGGGGAC CAGACAAAAA 360
90
91 AGGAATGGTG CAGAATTGTT AGGCGCACCT ACCAAAAGCA TCTTGCCTT TATTGCAAAG 420
92
93 ATAAAGCAGA TTCCTCTAGT ACAAGTGGGG AACAAAATAA CGTGGAAAAG AGCTGTCCTG 480
94
95 ACAGCCCAC TACTAATGCG TATGACGAAC GCAGTGACGA CCACAAAAGA ATTCCCTCTA 540
96
97 TATAAGAAGG CATTCAATTCC CATTGAGG ATCATCAGAT ACTAACCAAT ATTTCTC 597
98
99 (2) INFORMATION FOR SEQ ID NO:2:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/464,099

DATE: 05/19/2000
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100
 101 (i) SEQUENCE CHARACTERISTICS:
 102 (A) LENGTH: 1982 base pairs
 103 (B) TYPE: nucleic acid
 104 (C) STRANDEDNESS: double
 105 (D) TOPOLOGY: linear
 106
 107 (ii) MOLECULE TYPE: DNA (genomic)
 108
 109
 110 (ix) FEATURE:
 111 (A) NAME/KEY: CDS
 112 (B) LOCATION: 62..1426
 113
 114
 115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 116
 117 AAGCCCGCGT TCTCTCCGGC GCTCCGCCCG GAGAGCCGTG GATAGATTAA GGAAGACGCC 60
 118
 119 C ATG TCG CAC GGT GCA AGC AGC CGG CCC GCA ACC GCC CGC AAA TCC 106
 120 Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser
 121 1 5 10 15
 122
 123 TCT GGC CTT TCC GGA ACC GTC CGC ATT CCC GGC GAC AAG TCG ATC TCC 154
 124 Ser Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser
 125 20 25 30
 126
 127 CAC CGG TCC TTC ATG TTC GGC GGT CTC GCG AGC GGT GAA ACG CGC ATC 202
 128 His Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile
 129 35 40 45
 130
 131 ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC AAT ACG GGC AAG GCC ATG 250
 132 Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met
 133 50 55 60
 134
 135 CAG GCC ATG GGC GCC AGG ATC CGT AAG GAA GGC GAC ACC TGG ATC ATC 298
 136 Gln Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile
 137 65 70 75
 138
 139 GAT GGC GTC GGC AAT GGC GGC CTC CTG GCG CCT GAG GCG CCG CTC GAT 346
 140 Asp Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp
 141 80 85 90 95
 142
 143 TTC GGC AAT GCC GCC ACG GGC TGC CGC CTG ACC ATG GGC CTC GTC GGG 394
 144 Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly
 145 100 105 110
 146
 147 GTC TAC GAT TTC GAC AGC ACC TTC ATC GGC GAC GCC TCG CTC ACA AAG 442
 148 Val Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys
 149 115 120 125
 150
 151 CGC CCG ATG GGC CGC GTG TTG AAC CCG CTG CGC GAA ATG GGC GTG CAG 490
 152 Arg Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln

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153	130	135	140														
154																	
155	G TG	A AA	T CG	G AA	G AC	GG T	G AC	C GT	CT T	C CC	G TT	A CC	T TG	C GC	G G G	CC G	538
156	Val	Lys	Ser	Glu	Asp	Gly	Asp	Arg	Leu	Pro	Val	Thr	Leu	Arg	Gly	Pro	
157	145						150						155				
158																	
159	A AG	A CG	CC G	AC G	CC G	AT C	A CC	T AC	C G C	G T G	CC G	A T G	G CC	T CC	G CA	C AG	586
160	Lys	Thr	Pro	Thr	Pro	Ile	Thr	Tyr	Arg	Val	Pro	Met	Ala	Ser	Ala	Gln	
161	160						165						170			175	
162																	
163	G TG	A AG	T CC	G CC	G T G	C T G	C T C	G CC	C T C	A AC	A CG	CC C	GG C	A TC	A CG	634	
164	Val	Lys	Ser	Ala	Val	Leu	Leu	Ala	Gly	Leu	Asn	Thr	Pro	Gly	Ile	Thr	
165	180									185			190				
166																	
167	A CG	G TC	A TC	G AG	CC G	AT C	A TG	A CG	C G C	G AT	C AT	A CG	C CC	GG C	A TC	682	
168	Thr	Val	Ile	Glu	Pro	Ile	Met	Thr	Arg	Asp	His	Thr	Glu	Lys	Met	Leu	
169	195							200					205				
170																	
171	C AG	GG C	TT T	GG C	G CC	A AC	C TT	A CC	G TC	G AG	A CG	G AT	G CG	G AC	GG C	G TG	730
172	Gln	Gly	Phe	Gly	Ala	Asn	Leu	Thr	Val	Glu	Thr	Asp	Ala	Asp	Gly	Val	
173	210								215				220				
174																	
175	C CG	A CC	A TC	C G C	C T G	G AA	GG C	C G C	G G C	A AG	C TC	A CC	GG C	C AA	G TC	A TC	778
176	Arg	Thr	Ile	Arg	Leu	Glu	Gly	Arg	Gly	Lys	Leu	Thr	Gly	Gln	Val	Ile	
177	225					230					235						
178																	
179	G AC	G T G	CC G	GG C	G AC	CC G	T CC	T CG	A CG	G CC	T TC	CC G	CT G	G TT	G CG	G CC	826
180	Asp	Val	Pro	Gly	Asp	Pro	Ser	Ser	Thr	Ala	Phe	Pro	Leu	Val	Ala	Ala	
181	240						245				250			255			
182																	
183	C TG	CT T	G TT	CC G	GG C	T CC	G AC	G TC	ACC	AT C	CT C	A AC	G TG	CT G	AT G	A AC	874
184	Leu	Leu	Val	Pro	Gly	Ser	Asp	Val	Thr	Ile	Leu	Asn	Val	Leu	Met	Asn	
185	260								265				270				
186																	
187	CCC	A CC	C G C	A C C	GG C	CT C	A T C	C T G	A C G	CT G	C A G	G A A	A T G	GG C	G C C	G A C	922
188	Pro	Thr	Arg	Thr	Gly	Leu	Ile	Leu	Thr	Leu	Gln	Glu	Met	Gly	Ala	Asp	
189	275								280				285				
190																	
191	AT C	G A A	G T C	A T C	A A C	CC G	CG C	CT T	G C C	GG C	G G C	G A A	G A C	G T G	G C G	G A C	970
192	Ile	Glu	Val	Ile	Asn	Pro	Arg	Leu	Ala	Gly	Gly	Glu	Asp	Val	Ala	Asp	
193	290							295					300				
194																	
195	CT G	C G C	G T T	CG C	T C C	T C C	A C G	C T G	A A G	GG C	G T C	A C G	G T G	CC G	G A A	G A C	1018
196	Leu	Arg	Val	Arg	Ser	Ser	Thr	Leu	Lys	Gly	Val	Thr	Val	Pro	Glu	Asp	
197	305							310				315					
198																	
199	CG C	G C G	C C T	T C G	A T G	A T C	G A C	G A A	T A T	CC G	A T T	C T C	G C T	G T C	G C C	G C C	1066
200	Arg	Ala	Pro	Ser	Met	Ile	Asp	Glu	Tyr	Pro	Ile	Leu	Ala	Val	Ala	Ala	
201	320							325				330			335		
202																	
203	G C C	T T C	G C G	G A A	GG G	G C G	A C C	G T G	A T G	A A C	GG T	C T G	G A A	G A A	C T C	C G C	1114
204	Ala	Phe	Ala	Glu	Gly	Ala	Thr	Val	Met	Asn	Gly	Leu	Glu	Glu	Leu	Arg	
205	340									345				350			

**RAW SEQUENCE LISTING
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206 GTC AAG GAA AGC GAC CGC CTC TCG GCC GTC GCC AAT GGC CTC AAG CTC 1162
 207 Val Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu
 208 355 360 365
 209
 210 AAT GGC GTG GAT TGC GAT GAG GGC GAG ACG TCG CTC GTC GTG CGC GGC 1210
 211 Asn Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly
 212 370 375 380
 213
 214 CGC CCT GAC GGC AAG GGG CTC GGC AAC GCC TCG GGC GCC GCC GTC GCC 1258
 215 Arg Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala
 216 385 390 395
 217
 218 ACC CAT CTC GAT CAC CGC ATC GCC ATG AGC TTC CTC GTC ATG GGC CTC 1306
 219 Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu
 220 400 405 410 415
 221
 222 GTG TCG GAA AAC CCT GTC ACG GTG GAC GAT GCC ACG ATG ATC GCC ACG 1354
 223 Val Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr
 224 420 425 430
 225
 226 AGC TTC CCG GAG TTC ATG GAC CTG ATG GCC GGG CTG GGC GCG AAG ATC 1402
 227 Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile
 228 435 440 445
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 230 GAA CTC TCC GAT ACG AAG GCT GCC TGATGACCTT CACAATGCC ATCGATGGTC 1456
 231 Glu Leu Ser Asp Thr Lys Ala Ala
 232 450 455
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 234 CCGCTGCGGC CGGCAAGGGG ACGCTCTCGC GCCGTATCGC GGAGGTCTAT GGCTTCATC 1516
 235
 236 ATCTCGATAC GGGCCTGACC TATCGGCCA CGGCCAAAGC GCTGCTCGAT CGGGCCTGT 1576
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 238 CGCTTGATGA CGAGGCGGTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGCTCG 1636
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 240 ACCGGTCGGT GCTGTCGGCC CATGCCATCG GCGAGGCGGC TTCTGAAGATC CGGGTCATGC 1696
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 242 CCTCGGTGCG GCGGGCGCTG GTGAGGCGC AGCGCAGCTT TGCGGCGCGT GAGCCGGCA 1756
 243
 244 CGGTGCTGGA TGGACGCGAT ATCGGCACGG TGGTCTGCC GGATGCCCG GTGAAGCTCT 1816
 245
 246 ATGTCACCAGC GTCACCGGAA GTGCGCGCA AACGCCGCTA TGACGAAATC CTCGGCAATG 1876
 247
 248 GCGGGTTGGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGGACA 1936
 249
 250 TGGGTCGGGC GGACAGTCCT TTGAAGCCCG CCGACGATGC GCACCTT 1982
 251
 252
 253
 254 (2) INFORMATION FOR SEQ ID NO:3:
 255
 256 (i) SEQUENCE CHARACTERISTICS:
 257 (A) LENGTH: 455 amino acids
 258 (B) TYPE: amino acid

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/09/464,099**

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Original Text